

FIG. 1

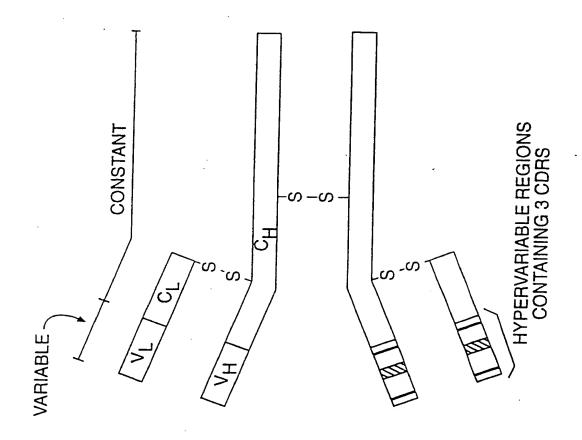


FIG. 2

EFFECT OF ANTI-STAPH MAB 96-110 ON SURVIVAL IN A LETHAL S.AUREUS SEPSIS MODEL

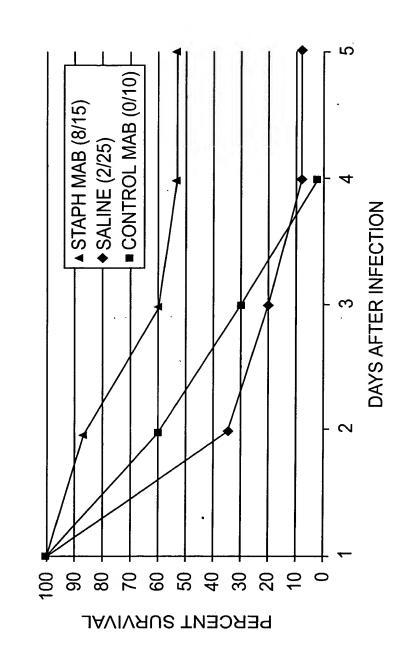


FIG. 3

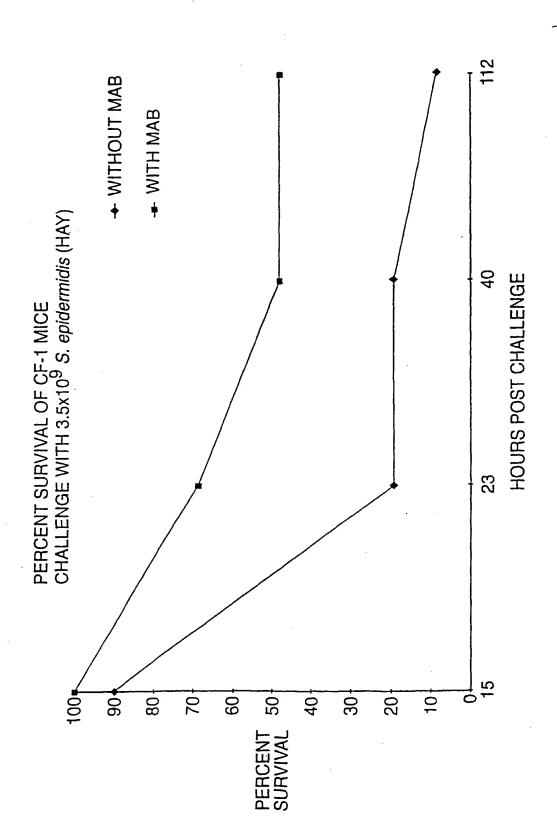


FIG. 4

6MER.SEQ				
	1,0	20	3,0	
				ano ma vio 4
41:13.6mer2-1	\		Y G A	SEQ ID NO.4
61	C A H	A D R V	TTATGGGGCC	SEQ ID NO.5
42:14.6mer2-2			Y G A	
65	G A H		•	,
43:15.6mer2-3	1	CGGATAGGGT A D R V	Y G A	
66	G A H			SEQ ID NO.6
44:16.6mer2-4			Y G A	SEQ ID NO.7
62	G ? H		TTATGGGGCC	PEG ID NO. /
45:17.6mer2-5	GGGGCTCATG	• • • • • • • • • • • • • • • • • • • •	Y G A	
67	G A H	A D R V	TTATGGGGCC	
46:18.6mer2-6	1			
68	G A H	A D R V	Y G A	
47:19.6mer2-7			TTATGGGGCC	
69	G A H	A D R V	Y G A	
48:20.6mer2-8	1	CCC	TTATGGGGCC	•
70	G A H	A D R V	Y G A	
49:21.6mer2-9	1	CGGATAGGGT	TTATGGGGCC	
71	G A H	A D R V	Y G A	
51:23.6mer2-11	ł			
72	G A H	A D R V	Y G A	
52:24.6mer2-12		CGGATAGGGT		
73	G A H	A D R V	Y G A	
53:25.6mer2-13	l-		TTATGGGGCC	
74	G A H	A D R V	Y G A	
54:26.6mer2-14		CGGATAGGGT	TTATGGGGCC	
75	G A H	A D R V	Y G A	
55:27.6mer2-15	i .	CGGATAGGGT	TTATGGGGCC	
76	G A H	A D R V	Y G A	
56:28.6mer2-16	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
77	G A H	A D R V	Y G A	
58:30.6mer2-18	GGGGCTCATG		TTATGGGGCC	
78	G A H	A D R V	Y G A	
59:31.6mer2-19	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
79	G A H	A D R V	Y G A	
60:32.6mer2-20	GGGGCTCATG	CGGATAGGGT	TTATGGGGCC	
80	G A H	A D R V	Y G A	

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i	

15MER2.SEQ										(
	10	20	30	40]		09			
50:07.15mer2-1/0	GGGCTTGGC	ATTGGCGTCA	TCGTATTCCT	CTTCAGCTTG	3CTG	ည	SEQ :		10.8	
	M V S	H W R H	R I P	r o r	A G	Ø	SEQ	U 0.	0.9	_
	GGGGCTCGTC	regra	TTTTTCTCAT	TTTTTTCATC	rcgi	ပ္ပ	SEQ	N 01	70.1	0
	G A R	z	<u>හ</u>	ъ,	S T	K	SEQ		10.1	-
53:10.15mer2-4/0	•	GCTTTGTT	TAGTCATTCT	TATCGTCCTC	GGGGTTCGGC	TGGGCCC	SEQ	101	0.1	[2]
73	<u>、</u>	E	_	3	ග	Ø	SEO	ID	NO.1	13
54:11.15mer2-5/0	ည္ဟ	TGGCGTCA	'ATT	CAGG	GCTGGTC	ပ္ပ	SEQ	_	10.1	14
74	~	X	⊢⊣	ŏ	A G	Ø	SEQ	101	NO.1	15
56:13.15mer2-7/0	ည္ဟ	TGGCGT	'ATT(CAG	GCTC	ည္ဟင္ပ	SEQ	1 QI	NO.1	16
1 2 9	>	N N	Н	ø	A G	A	SEQ	ID	NO.1	17
57:14.15mer2-8/0		TGGCGT	'ATT	CAG	GCTGGT	TGGGGCC	SEQ	_	0.0	18
77 G A W		X X		Ŏ	A G	G A	SEQ	ID	VO.1	19
58:15.15mer2-9/0	GGGCCTCAGG	SCTGTT	CCT	GCTC	ACTGAG	TGGGGCC	SEQ	_	VO.2	20
78	G A D	A V	Д	Ø	딘	GA	SEQ	_	30.2	21
59:16.15mer2-10/0	GGGCTCGTC	SATGGT	TCT	TTT(TCGTTC	TGGGGCC	SEQ	_	NO.2	22
79	G A R	E H	တ	[Z,	S	G B	SEQ		80.2	23
60:17.15mer2-11/0	GGGCTCGTC	SATGGT	TCT	TTT(TCGTTC	TGGGGCC	SEQ		•	24
80	G A R	R H G N	F S H	F F H	വ	A D	SEO	_	NO.2	25
61:18.15mer2-12/0	GGGCCTTGGC	ATGTAT	CAT	900	CGTAGT	TGGGGCC	SEQ		•	26
81 G A (W)	G A W	M		~	× S	G A	SEQ		•	27
62:19.15mer2-13/0	GGGCCTTGGC	ATGTAT	CAT	929	CGTZ	TGGGGCC	SEQ		_•	28
82	G A W	M	H	Ø	S	G A	SEQ		 8	29
63:20.15mer2-14/0	GGGCTTGGC	AAGTATT	TAT	SCG	<i>PTGTAGT</i>	TGGGGCC	SEQ		_•	30
83	G A	M		H A H	ပ	G B	SEQ		_•	31
64:21.15mer2-15/0	GGGCTTGGC	ATGTATT	TCAT	၁၅၁၅	AGTC	TGGGGCC	SEQ	ΠΩ	 S	32
84	G A	R M Y F		н А н	×	G	SEQ	OI OI	``. Q	33
65:22.15mer2-16/0 GGGGCTT	GGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATGCGCATC		ည္ဟ	SEQ		g	34
85	G A W	R M Y F	S H R	•		A	SEO	al	2	35

15MER2.SEQ			-00					
	10	20	30	40	50		09	
66:23.15mer2-17/0 GGGGCTTGGC GTATGTATTT TTCTCATCGT CATGCGCATC TTCGTAGTCC TGGGGCCC	GGGCTTGGC	GTATGTATTT	TTCTCATCGT	CATGCGCATC	TTCGTAGTCC	TGGGGCC	SEQ ID NO.36	.36
98	G A W	R M Y F	S H R	H A H	L R S P	G A	SEQ	.37
67:24.15mer2-18/0 GGGGCTCGTC GGCATGGTAA TTTTTCTCAT	GGGGCTCGTC	GGCATGGTAA	TTTTTCTCAT	TTTTTCATC	TTTTTTCATC GGTCGTTGAT TGGGGCC	TGGGGCC	ID	.38
87	G A H	R H G N	F S H	F F H	R S L I	G A	Π	.39
68:25.15mer2-19/0 GGGGCTTGGC ATTGGCGTCA TCGTATTCCT	GGGCTTGGC	ATTGGCGTCA	TCGTATTCCT	CTTCAGCTTG	CTTCAGCTTG CTGCTGGTCG TGGGGCC	TGGGGCC	Π	0.40
88	CAW	H W R H	R I P	7 Ö 7	A A G R	G A	11	NO.41
69:26.15mer2-20/0 GGGGCTCGTC GGCATGGTAA TTTTTCTCAT TTTTTCATC GGTCGTTGAT TGGGGCC	GGGCTCGTC	GGCATGGTAA	TTTTTCTCAT	TTTTTCATC	GGTCGTTGAT	TGGGGCC	SEQ ID NO	NO.42
68	G A H	R H G N F S H	F S H	म म	R S L I G A	G G	Π).43

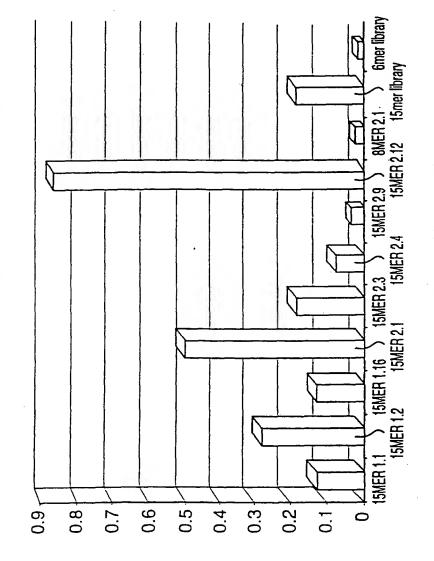
	D NO.45 D NO.45 D NO.45 D NO.47	ID NO.48 ID NO.49
09	SEQ 11 SEQ 11 SEQ 11 SEQ 11	SEQ I SEQ I
	TGGGGCC G A	2 1766 1766 1766
50	V L V L V L V L V L V L V L V L V L V L V L V L V L V L V L V L V L V L TGTTCTTT TGTTCTTT	R V L S GGGGTTCGGC R G S A GTGTTCTTTC R V L S
40	CATGATC (H) D CCATGATC H D	H D CGTCATC R (H) CATGATC
30	CGTCGT R R CGTCGT R R CGTCGT R R CGTCGT R R CCGTCGT R R R R R CCGTCGT R R R R R CCGTCGT R R R R CCGTCGT R R R R R R CCGTCGT R R R R R R R R R R R R R R R R R R R	
20	ACTIT ACTIT T F ACTIT A	
10	I 🔾	3A IT
	51:28.15mer1-2/0 GGGGCTGATT 67 6 A D 68 68 65 62:13.15mer1-6/0 GGGGCTGGTT 65 62:13.15mer1-6/0 GGGCTGGTT 66 63:14.15mer1-9/0 GGGCTGGTT 68 6 A D 64:15.15mer1-10/0 GGGCTGGTT 68 6 A D 65:16.15mer1-10/0 GGGCTGGTT 69 65:16.15mer1-11/0 GGGCTGGTT 70 6 A D 56:17.15mer1-11/0 GGGCTGGTT 71 6 A D 57:28.15mer1-11/0 GGGCTGGTT 72 6 A D 59:20.15mer1-11/0 GGGCTGGTT 73 6 A D 69:20.15mer1-11/0 GGGC	74 71:22.15mer1-16/0 GGGGCTC 75 G A 72:23.15mer1-17/0 GGGGCTC
	51:28 67 68 65.13 66 63:14 67 68 69 69 69 70 70	74 71:22. 75 72:23.

FIG. 7A

15MER1.SEQ					-	
	10	20	30	40	. 50	09
73:24.15mer1-18/0 GGGGCTGGTT CGATTACTTT TCATCGTCGT CATCATGATC GTGTTCTTTC TGGGGCC	GGGCTGGTT	CGATTACTTT TCATCGTCGT	TCATCGTCGT	CATCATGATC	CATCATGATC GTGTTCTTTC TGGGGC	TGGGGCC
74:25.15mer1-19/0 GGGGCTGGTT	GGGCTGGTT		TCATCGTCGT	CATCATGATC	CGATTACTIT TCATCGTCGT CATCATGATC GIGTICITIC TGGGGCC	TGGGGCC
78	G A D	W I T F	H R R		H H D R V L S G A	G A
75:26.15mer1-20/0 GGGCTGGT	GGGCTGGTT		TCATCGTCGT	CATCATGATC	CGATTACTIT TCATCGTCGT CATCATGATC GTGTTCTTTC TGGGGCC	TGGGGCC
13	G A D	WITF	H R R	п н	H R R H H D R V L S	G A

51:15mer 1st.1 GGGGCTGATT CGATTACTTT TCATCGTGGT CGTCTTTC TGGGGCC 16/17 SEQ 1D N 57 G A D W I T F H R R H H D R V L S G A SEQ 1D N 59 15mer 1st.2 GGGGCTGAGT GTCATATGCT TGCTGTTTC TGGGGCC 1/10 SEQ 1D N 59 15mer 1st.16 GGGCTGGGA AGCTATGTTTC TGTCGGTCG TGGGGCC 1/17 SEQ 1D N 6 A S R H M L A R R W S R L L A V P G A SEQ 1D N 92 15mer 2nd.1 GGGCTTGGC ATTGGCGTCA TGTCTGTTTC TTCTCTCATC GGCGTCGGCC 1/17 SEQ 1D N 6 A W R H R I P L Q L A G R G S GGGTTGGGC 5/18 SEQ 1D N 98 15mer 2nd.1 GGGCTTGGT ATTGTTTCTCAT TTTTTTCATC GGTCTGGTC 6/18 SEQ 1D N 93 15mer 2nd.3 GGGCTTGGT ATTGTTTTTTTCAT GGTCTTTTTTTTCATC GGTCTTGGT TGGGGCC 1/18 SEQ 1D N 6 A R R H G N F S H F F H R S L I G A SEQ 1D N 99 100 G A W X A L F S H S Y R P R G S A G A SEQ 1D N 6 G A W X A L F S H S Y R P R G S A G A SEQ 1D N 95 15mer 2nd.9 GGGCTTGGT TGGCTTTTTTTTTTTTTTTTTTTTTTTT	masterlist	ist					•				
GATTACTTT TCATCGTCGT CATCATGATC GTGTTCTTTC TGGGGCC 16/17 SEQ 1D 17 F H R R H H D R V L S G A SEQ 1D 17 SEQ 1D 17 SEQ 1D 17 SEQ 1D 18 SEQ			10		30	40	50		09	70	
I	51:15me	r 1st.1	GGGCCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	16/17	SEQ II	NO.5
TYCATATGCT TGCTCGGTGG TCGCGTTTGC TTGCTGTTTC TGGGGCC 1/10 SEQ ID INCCTATATGCT TATCGTCATC GGCGTTCGGC TGGGGCC 1/17 SEQ ID INCGCTATGTT TAGTCATTCT TATCGTCATC GGCGTTCGGC TGGGGCC 1/17 SEQ ID INCGCGTCA TCGTATTCCTCT CTTCAGCTTG CTGCTGGTCG TGGGGCC 5/18 SEQ ID INCGCTGGTAA TTTTTCTCAT TTTTTTCATC GGTCGTTGAT TGGGGCC 6/18 SEQ ID INCGCTTGTT TAGTCATTCT TATCGTCCTC GGGGTTCGGC TGGGGCC 1/18 SEQ ID INCGCTGTTTT TAGTCATTCT TATCGTCCTC GGGGTTCGGC TGGGGCC 1/18 SEQ ID INCGCTGTTTT TAGTCATTCT TATCGTCATG CTACTGAGCT TGGGGCC 1/18 SEQ ID INCGCTGTTTT TTTCTCATCGT TATCGCTGATG CTACTGAGCT TGGGGCC 1/18 SEQ ID INCGCTGTTTT TTTCTCATCGT TTTGGCTGATG CTACTGAGCT TGGGGCC 6/18 SEQ ID INCGGGTGTTTT TTTCTCATCGT TTTGGCTGATG CTACTGAGCT TGGGGCC 6/18 SEQ ID INCGGGTTTTT TTTCTCATCGT TTTGGCTGATG CTACTGAGCT TGGGGCC 6/18 SEQ ID INCGGGTTTTT TTTCTCATCGT TTTGGCTGATG CTACTGAGCT TGGGGCC 6/18 SEQ ID INCGGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	57		G A D	TI	×	Ξ	N L			SEQ II	0 NO.5
GGCTATGTT TAGTCATTCT TATCGTCATC GGCGTTCGGC TGGGGCC 1/17 SEQ ID INCREMENTAL TAGTCATTCT TATCGTCATC GGCGTTCGGC TGGGGCC 1/17 SEQ ID INCREGGTCA TCGTATTCCT CTTCAGCTTG CTGCTGGTCG TGGGGCC 5/18 SEQ ID INCREGGTCA TCGTATTCTCAT TTTTTCATC GGTCGTTGAT TGGGGCC 6/18 SEQ ID INCREGGTA TTTTTTCTCAT TATCGTCGTCG GGGGTTCGGC G/18 SEQ ID INCREGGTTTTT TAGTCATTCT TATCGTCGTCG GGGGTTCGGC TGGGGCC 1/18 SEQ ID INCREGGTTTTT GTATCCTCCT TTGGCTGATG CTACTGAGCT TGGGGCC 1/18 SEQ ID INCREGGTTTTT GTATCCTCCT TTGGCTGATG CTACTGAGCT TGGGGCC 1/18 SEQ ID INCREGGTTTTT TTCTCATCGT TTGGCTGATG TTCTCATGGCGCT TTGGCGCC 6/18 SEQ ID INCREGGTTTTT TTCTCATCGT TTGGCGCT TTGGGGCC 6/18 SEQ ID INCREGGTTTTT TTCTCATCGT TTGGCGCT TTGGGGCC 6/18 SEQ ID INCREGGTTTTTTCTCATCGT TTGGCGCC 1/18 SEQ ID INCREGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	90 15mei	r 1st.2	GGGCCTAGTC	TCATATE	TGCTCGG	TCGCGTTTGC	GTTT	TGGGGCC	1/10	SEQ II	NO.5
GGCTATG'TT TAGTCATTCT TATCGTCATC GGCGTTCGGC TGGGGCC 1/17 SEQ 1D 12 L A B G A G A SEQ 1D 12 L Q L A A G R G A SEQ 1D 12 L Q L A A G R G A SEQ 1D 12 L Q L A A G R G A SEQ 1D 12 L Q L A A G R G A SEQ 1D 12 L Q L A A G R G A SEQ 1D 12 L Q L A A G R G A SEQ 1D 12 L Q L A A G R G A SEQ 1D 12 L Q L A A G R G A SEQ 1D 12 L Q L A L R S L I G A SEQ ID 12 L Q L A L R S L I G A SEQ ID 12 L Q L A L R S L R G S A G A SEQ ID 12 L A L R S L R G S A G A SEQ ID 12 L A L R S L R G S A G A SEQ ID 12 L A L R R L R R G S A G A SEQ ID 12 L A L R R R R L R R R R R R R R R R R R	91		S A S	H H	œ	ĸ	A V	G B		SEQ II	0 NO.5
TTGGCGTCA TCGTATTCCT CTTCAGCTTG CTGCTGGTCG TGGGGCC	71:15me	r 1st.16	GGGCCTGGGA	GGCTATGI	CAT	CGTCA'	GGCGTTCGGC	TGGGGCC	1/17	SEQ II	0 NO.5
15mer 2nd.1 GGGGCTTGGC ATTGGCGTCA TCGTATTCCT CTTCAGCTTG CTGCTGGTCG TGGGGCC 5/18 SEQ ID 1 G A W H W R H R I P L Q L A A G R G A SEQ ID 1 SEQ ID 1 G A R R H G N F S H F F H R S L I G A SEQ ID 1 G A W X A L F S H S Y R P R G S A G A SEQ ID 1 Sex 2nd.4 GGGGCTTGGA AGGCTTTGTT TAGTCATTCT TATCGTCCTC GGGGTTCGGC TGGGGCC 1/18 SEQ ID 1 Sex 2nd.9 GGGGCTTGGA GGCTTTGTT TAGTCATTCT TATGGCTTGATG CTACTGAGCT TGGGGCC 1/18 SEQ ID 1 Sex 2nd.12 GGGGCTTGGC GTATGTATTT TTCTCATCGT CATGCGCATC TTCGTAGTCC TGGGGCC 6/18 SEQ ID 1 G A W R M Y F S H R H A H L R S P G A SEQ ID 1 GGGCTTGTC GGGGCCC 6/18 SEQ ID 1 GGGCTTGTC GGGGCCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCC TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCC TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTTGTAG CGGATAGGCT TTATGGGCGC 7 TGGGGCC 6/18 SEQ ID 1 GGGCTTGTAG CGGATAGGCT TTATGGGCC 6/18 SEQ ID 1 GGGCTTGTAG CGGTTGTAG CGGTTGTAG CGGTTGTAG CGGTTGTAG CGGGCT 1 TATGTAG CGGTTGTAG CGGGTTGTAG CGGGCT 1/18 SEQ ID 1 GGGCTTGTAG CGGTTGTAG CGGGTTGTAG CGGGTTGTAG CGGGCT 1/18 SEQ ID 1 GGGTTGTAG CGGGTTGTAG CGGGTTGT	85		G A G	A M	S H S	R H	R G S A	G G		SEQ II	D NO.5
15mer 2nd.3 GGGCTCGTC GCCATGGTAA TTTTTCTCAT TTTTTCATC GGTCGTTGAT TGGGCC 6/18 SEQ ID 15 GGGCTTGGA GGCTTTGTT TATCGTCCTC GGGGTTCGGC TGGGGC 6/18 SEQ ID 15 G A W X A L F S H S Y R P R G S A G A SEQ ID 15 G A Q V A V L Y P P L A D A T E L G A SEQ ID 15 G A W R M Y F S H R H A H L R S P G A SEQ ID 15 G A W R M Y F S H R H A H L R S P G A SEQ ID 16 G A W R M Y F S H R H A H L R S P G A SEQ ID 16 G A W R M Y F S H R H A H L R S P G A SEQ ID 17 GGGCTCATG CGGATAGGGT TTATGGGGCC TGGGGCC 6/18 SEQ ID 18/18 SEQ ID 18/18/18 SEQ ID 18/18			GGGCCTTGGC	ATTGGCGT	TCGTATTCCT	CAGCT	CTGCTGGTCG	TGGGGCC	5/18	SEQ I	D NO.5
15mer 2nd.3 GGGGCTCGTC GGCATGGTAA TTTTTCTCAT TTTTTTCATC GGTCGTTGAT TGGGGCC 6/18 SEQ ID 1 G A R R H G N F S H F F H R S L I G A SEQ ID 1 G A W X A L F S H S Y R P R G S A G A SEQ ID 1 G A W X A L F S H S Y R P R G S A G A SEQ ID 1 G A Q V A V L Y P P L A D A T E L G A SEQ ID 1 G A Q V A V L Y P P L A D A T E L G A SEQ ID 1 G GGCTTGC GTATGTATTT TTCTCATCGT CATGCGCATC TTCGTAGTC TGGGGCC 6/18 SEQ ID 1 G A W R M Y F S H R H A H L R S P G A SEQ ID 6 A SEQ ID 6 A SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 GGGGCC 7 GGGGCC 6/18 SEQ ID 6 A B D R V Y G A SEQ ID 6 A SEQ ID 1 GGGCTCATG CGGATAGGCT TTATGGGGCC 7 GGGGCC 7 GGGGCC 6/18 SEQ ID 6 A B D R V Y G A SEQ ID 6 A S			M C C	H W R		7 0	A A G R	e C		SEQ_II	D NO.57
15mer 2nd.4 GGGCTTGGA AGCTTTGTT TAGTCATTCT TATCGTCCTC GGGGTTCGC TGGGGCC 1/18 SEQ ID 1 G A W X A L F S H S Y R P R G S A G A SEQ ID 1 G A W X A L F S H S Y R P R G S A G A SEQ ID 1 G A Q V A V L Y P P L A D A T E L G A SEQ ID 1 Smer 2nd.12 GGGCTTGGC GTATGTATTT TTCTCATCGT CATGCGCATC TTCGTAGTCC TGGGGCC 6/18 SEQ ID 1 G A W R M Y F S H R H A H L R S P G A SEQ ID 1 G A H A D R V Y G A SEQ ID 1 SEQ ID 1 GGGCTCATG CGGATAGGGT TTATGGGGCC			GGGCTCGTC	GGCATGGTAA	TTTTCT	PTTCA'	GGTCGTTGAT	TGGGGCC	6/18	SEQ II	D NO.58
15mer 2nd.4 GGGGCTTGGA AGGCTTTGTT TAGTCATTCT TATCGTCCTC GGGGTTCGGC TGGGGCC 1/18 SEQ ID 1 G A W X A L F S H S Y R P R G S A G A SEQ ID 1 SEQ ID 1 GGGCTCAGG TGGCTTTT GTATCCTCCT TTGGCTGATG CTACTGAGCT TGGGGCC 1/18 SEQ ID 1 Sec ID 1 GGGCTTGGC GTATGTATTT TTCTCATCGT CATGCGCATC TTCGTAGTCC TGGGGCC 6/18 SEQ ID 1 GGGCTCATG CGGATAGGGT TTATGGGGCC			G A R	R H G N	F S H	F F H	R S L I	A S		SEQ I	D NO.59
15mer 2nd.9 GGGCTCAGG TGCTGTTTT GTATCCTCCT TTGGCTGATG CTACTGAGCT TGGGGCC 1/18 SEQ ID IS A Q V A V L Y P L A D A T E L G A SEQ ID IS GGGCTTGGC GTATGTATTT TTCTCATCGT CATGCGCATC TTCGTAGTCC TGGGGCC 6/18 SEQ ID IS A W R M Y F S H R H A H L R S P G A SEQ ID GGGCTCATG CGGATAGGGT TTATGGGGCC SEQ ID IS SEQ ID IS A B B R V Y G A SEQ ID IS SEQ ID			GGGCCTTGGA	AGGCTTTGTT	TAGTCATTCT	TATCGTCC	GGGGTTCGGC	TGGGGCC	1/18	SEQ I	D NO.6
15mer 2nd.9 GGGGCTCAGG TGGCTGTTTT GTATCCTCCT TTGGCTGATG CTACTGAGCT TGGGGCC 1/18 SEQ ID G A Q V A V L Y P P L A D A T E L G A SEQ ID 15mer 2nd.12 GGGGCTTGGC GTATGTATTT TTCTCATCGT CATGCGCATC TTCGTAGTCC TGGGGCC 6/18 SEQ ID G A W R M Y F S H R H A H L R S P G A SEQ ID 6mer 2nd.1 GGGCTCATG CGGATAGGGT TTATGGGGCC SEQ ID G A H A D R V Y G A SEQ ID SEQ ID			G A W	X A L	SHS	Y R P	R G S A	G B		SEQ I	D NO.61
G A Q V A V L Y P P L A D A T E L G A SEQ ID 15mer 2nd.12 GGGGCTTGGC GTATGTATTT TTCTCATCGT CATGCGCATC TTCGTAGTCC TGGGGCC 6/18 SEQ ID G A W R M Y F S H R H A H L R S P G A SEQ ID 6mer 2nd.1 GGGGCTCATG CGGATAGGGT TTATGGGGCC SEQ ID G A H A D R V Y G A SEQ ID	95 15me:	r 2nd.9	GGGCTCAGG	TGGCTGTTTT	GTATCCTCCT	TTGGCTGA	CTACTGAGCT	TGGGGCC	1/18	SEQ I	D NO.6
15mer 2nd.12 GGGGCTTGGC GTATGTATTT TTCTCATCGT CATGCGCATC TTCGTAGTCC TGGGGCC 6/18 SEQ ID G A W R M Y F S H R H A H L R S P G A SEQ ID 6mer 2nd.1 GGGGCTCATG CGGATAGGGT TTATGGGGCC G A H A D R V Y G A			G A Q	V A V L	У Р Р	LAD	ATEL	A G		SEQ I	D NO.6
6mer 2nd.1 GGGGCTCATG CGGATAGGGT TTATGGGGCC 18/18 SEQ ID G A B C SEQ ID SEQ ID G A B C V Y G A SEQ ID		r 2nd.12	GGGCTTGGC		TTCTCAT	CATGCGCA	TTCGTAGTCC	Ō	6/18	SEQ I	D NO.6
6mer 2nd.1 GGGGCTCATG CGGATAGGGT TTATGGGGCC 18/18 SEQ ID G A H A D R V Y G A SEQ ID			G . A W		SH	H A	လ			SEQ I	D NO.6
G A H A D R V Y G A		r 2nd.1	GGGCCTCATG	_	TTATGGG				18/18	SEQ I	D NO.66
			A	D	5					SEQ I	D NO.67

COMPARISON OF SIGNALS AT 6.25x10" virus/mL



3RD ROUND ISOLATES

FIG. 9

GENERAL CLONING STRATEGY

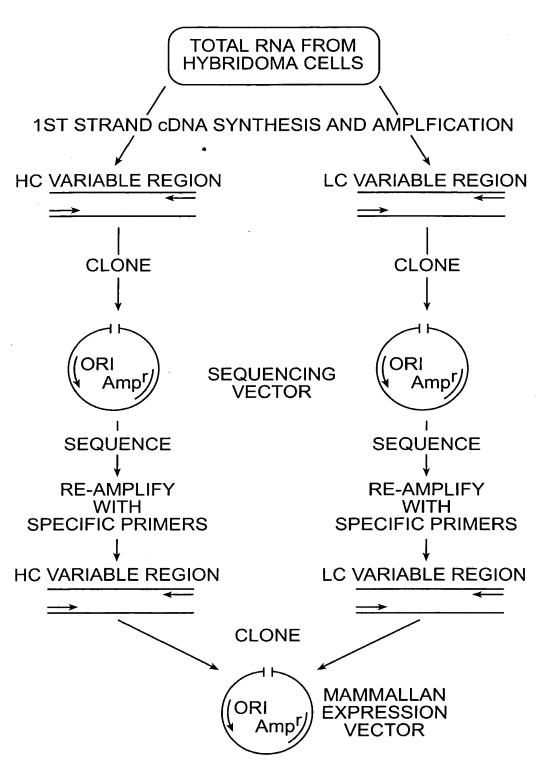


FIG. 10

MOUSE HEAVY CHAIN "FRONT" PRIMERS

TSS1

SEQ ID NO.68 5'-ATTTCAGGCCCAGCCGGCCATGGCCGARGTRMAGCTKSAKGAGWC-3'

SEQ ID NO.69 5'-ATTTCAGGCCCAGCCGGCCATGGCCGARGTYCARCTKCARCARYC-3' 5'-ATTTCAGGCCCAGCCGGCCATGGCCCAGGTGAAGCTKSTSGARTC-3' SEQ ID NO.70

5'-ATTTCAGGCCCAGCCGGCCATGGCCGAVGTGMWGCTKGTGGAGWC-3' SEQ ID NO.71

5'-ATTTCAGGCCCAGCCGGCCATGGCCCAGGTBCARCTKMARSARTC-3' SEQ ID NO.72

MOUSE HEAVY CHAIN "BACK" PRIMERS

JS16(

SEQ ID NO.73 5'-GCTGCCACCGCCACCTGMRGAGACDGTGASTGARG-3' SEQ ID NO.74 5'-GCTGCCACCGCCACCTGMRGAGACDGTGASMGTRG-3' 5'-GCTGCCACCGCCACCTGMRGAGACDGTGASCAGRG-3' SEQ ID NO.75

FIG. 11A

MOUSE LIGHT CHAIN LEADER "FRONT" PRIMERS

5'-CCCGGGCCACCATGGAGACAGACACTCCTG-3' SEQ ID NO.76

5'-CCCGGGCCACCATGGATTTTCAAGTGCAGATTTTC-3' SEQ ID NO.77

5'-CCCGGGCCACCATGGAGWCACAKWCTCAGGTC-3' SEQ ID NO.78

5'-CCCGGGCCACCATGKCCCCWRCTCAGYTTCTKG-3' SEQ ID NO.79

5'-CCCGGGCACCATGAAGTTGCCTGTTAGGCTG-3' SEQ ID NO.80

FIG. 11B

MOUSE LIGHT CHAIN "BACK" PRIMER

5'-GCACCTCCAGATGTTAACTGCTC-3' SEQ ID NO. 81

"96-110" SPECIFIC PRIMERS

96110HF2

5'-TAATA<u>TCGCGA</u>CAGCTACAGGTGTCCACTCCCGAAGTGATGCTGGTGGAGWCTG-3' SEQ ID NO.82

96100HB 5'-TTATA<u>GAATTC</u>TGAGGAGACGGTGAGTGAG-3' SEQ ID NO.83

96110BLF

5'-TTAGGCGATAGCGTTCTCTCCCAGTCTCC-3' SEQ ID NO.84

96110BLB

5'-GTAACCG TTCGAAAAGTGTACTTACGTTTTATTTCCAGCATGGTCC-3' SEQ ID NO.85

96-110 ANTI-STAPH (HAY) HEAVY CHAIN VARIABLE REGION (TYPE IIIA)

GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCTCATGTGCAGCCTCTGGATTTCACCTTCAAT Ö വ ø ď ی വ ப × ᆸ വ G × Д Ø Λ 1 ט C ט ഗ ഥ ᆸ M A

AACTACGCCATGAAT TGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCT N Y A M N W V R Q A P G K G L E W V A

CGCATAAGAAGTAAATAATTATGCAACATTTTATGCCGATTCAGTGAAAGAC R I R S K S N N Y A T F Y A D S V K D AGGTTCACCATCTCCAGAGATGATTCACAAAGCATGCTCTATCTGCAAATGAACAACTTGAAAACTGAGAGACACAGCCATGTATTACTGTGTGAGA ď 四 ⊢ ப z N W Ŏ 口 ΙΛ Σ വ Ŏ മ Д

CGGGGGGCTTCAGGGATTGACTATGCTATGGACTAC TGGGGTCAAGGAACCTCACTCACCGTCTCCTCA SEQ ID NO. 86 R G A S G I D Y A M D Y W G Q G T S L T V S S SEQ ID NO. 87

FIG. 12A

96-110 ANTI-STAPH (HAY) LIGHT CHAIN VARIABLE REGION (TYPE VI)

CAAATTGTTCTCCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAAAAGGTCACAATGACTTGC ø വ ப ø വ ഗ

AGGGCCAGCTCAAGTGTAAATTACATGCAC R A S S V N Y M H TGGTACCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTCT GCCACATCCAACCTGGCTTCT Д വ Ö പ Ø GGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGC Ø 臼 വ ᆸ တ വ ₽ Ö വ ט വ ෆ മ α ø

CAGCAGTGGAGTAGTAACCCACCACG TTCGGAGGGGGGGCACCATGCTGGAAATAAGA SEQ ID NO. 88 Q Q W S S N P P T P G G G T M L E I R SEQ ID NO. 89

CDR REGIONS UNDERLINED

FIG. 12B

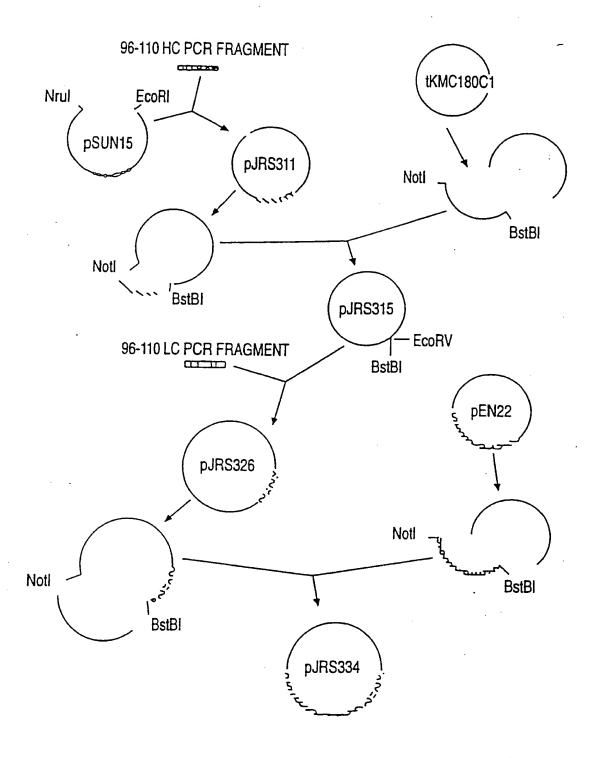
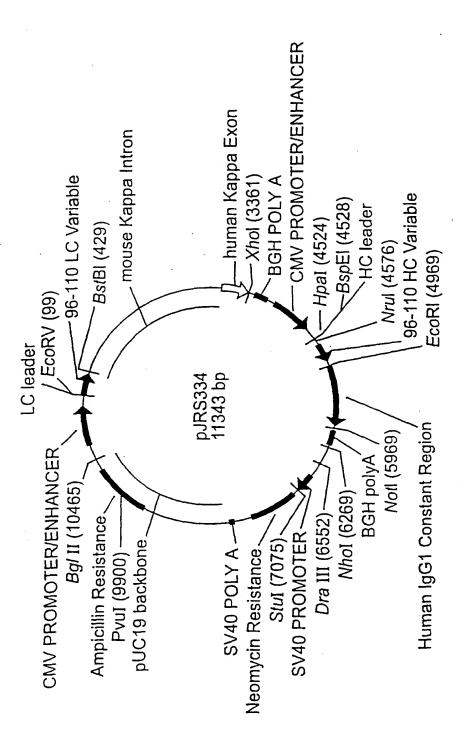


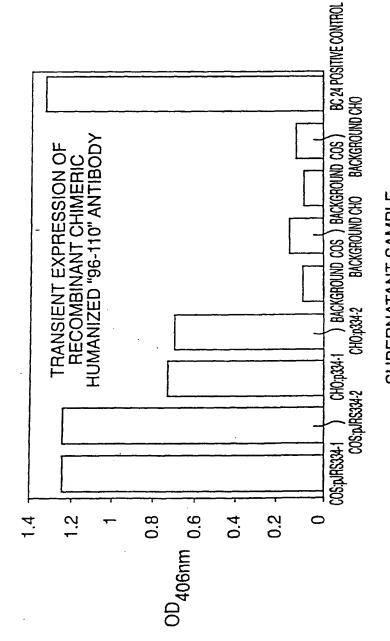
FIG. 13



Common Unique Restriction Sites Shown

FIG. 14

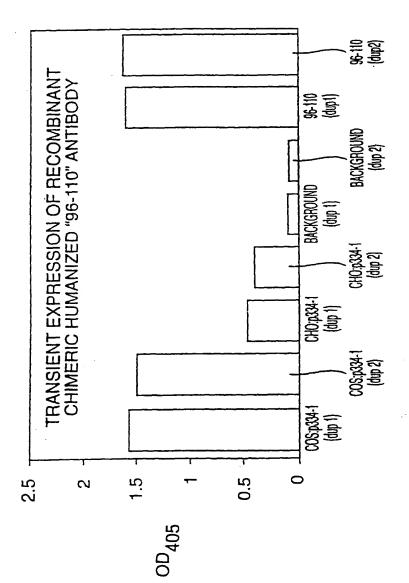
ANTIBODY PRODUCTION ELISA



SUPERNATANT SAMPLE

FIG. 15





SUPERNATANT SAMPLE

FIG. 16

OPSONIC ACTIVITY OF HUMAB 96-110 FOR S.EPIDERMIDIS IN A NEUTROPHIL MEDIATED OPSONOPHAGOCYTIC BACTERICIDAL ASSAY USING HUMAN COMPLEMENT

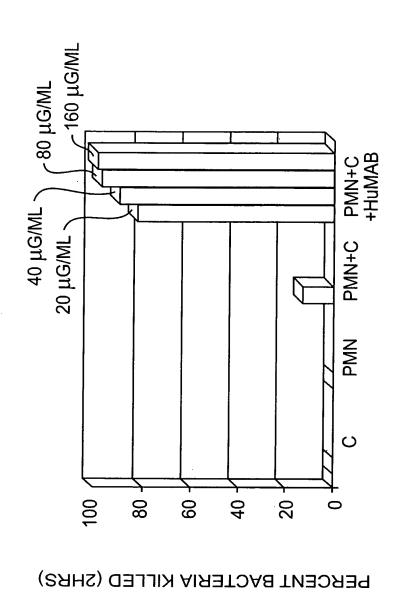
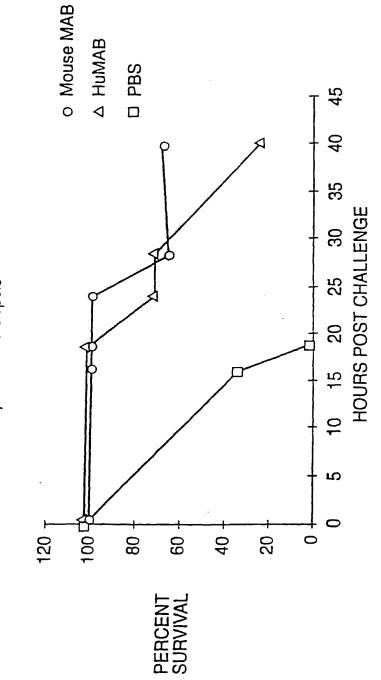


FIG. 17

BACTERIA-S. EPIDERMIDIS (STRAIN HAY)

C- BACK-EX (1:D), HUMAN PMN-HUMAN

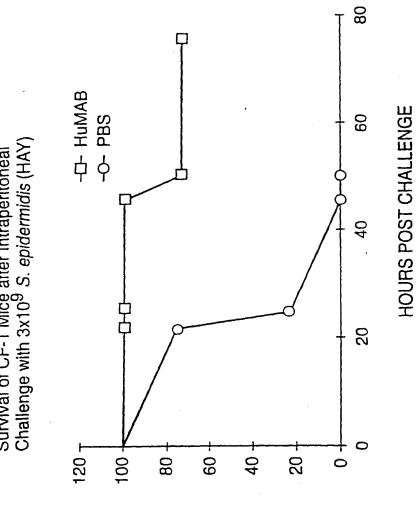
Pilot Study to Compare the Effect of Mouse MAB 96-110 and HuMAB 96-110 in a Lethal Model of S. epidermidis Sepsis



MAB dose: 14 mg/kg given IP, 24 and 1 hour prior to infection

FIG. 18

Survival of CF-1 Mice after Intraperitoneal Challenge with 3x109 S. epidermidis (HAY)



PERCENT SURVIVAL

18 mg/kg/dose, IP, 24 and 1 hour prior to infection

FIG. 19

Effect of HuMAB 96-110 on Bacteremia in a Lethal S. epidermidis Sepsis Model

Geometric Mean Bacteremia Level

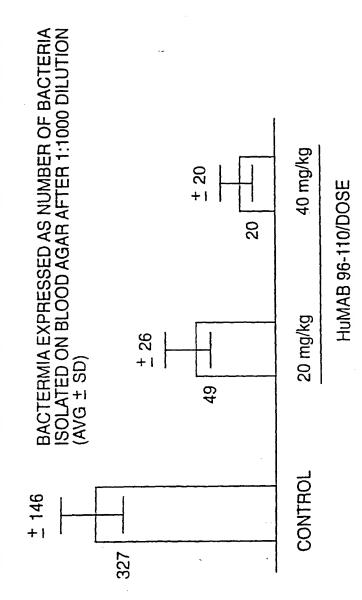
7 × 103	1.7 x 101	18 hrs
5.2 x 104	2.1 × 101	12 hrs
7.2 x 104	7.5 x 102	8 hrs
6.5 x 104	3 × 102	4 hrs
Saline Placebo	HuMAB 96-110	

Time Post Infection

HuMAB 96-110 18 mg/kg/dose or saline given IP, 24 and 1 hour prior to IP infection with 3x109 S. epidermides (Hay)

FIG. 20

BACTEREMIA LEVELS 4 HRS AFTER INFECTION WITH 3X109 S. EPIDERMIDIS*



*CF-1 MICE INFECTED IP WITH STRAIN HAY-HUMAB GIVEN IPx2

FIG. 21

The Effect of Hu 96-110 on Survival in a Lethal Neonatal *S. epidermidis** Sepsis Model

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